

Resource Summary Report

Generated by T1D on Jul 29, 2026

NanoporeTech: GridION Mk1

RRID:SCR_017986

Type: Tool

Proper Citation

NanoporeTech: GridION Mk1 (RRID:SCR_017986)

Resource Information

URL: <https://nanoporetech.com/products/gridion>

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Description: Benchtop sequencing and analysis device designed to run and analyse up to five individually addressable MinION or Flongle Flow Cells by Oxford Nanopore Technologies. Good for labs with multiple projects that need advantages of nanopore sequencing: simple library preparation, real-time analysis and new biological insights from long reads.

Resource Type: instrument resource

Keywords: sequencing machine, hardware, high-throughput sequencing, instrument, equipment

Availability: Restricted

Specification URL: https://raw.githubusercontent.com/SciCrunch/RRID-Instruments/main/PDF/SCR_017986.pdf

Resource Name: NanoporeTech: GridION Mk1

Resource ID: SCR_017986

Alternate URLs: https://community.nanoporetech.com/requirements_documents/gridion-mk1-spec.pdf

Record Creation Time: 20220129T080338+0000

Record Last Update: 20260725T190842+0000

Ratings and Alerts

No rating or validation information has been found for NanoporeTech: GridION Mk1.

No alerts have been found for NanoporeTech: GridION Mk1.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Wright DJ, et al. (2022) Long read sequencing reveals novel isoforms and insights into splicing regulation during cell state changes. BMC genomics, 23(1), 42.

Zhang R, et al. (2021) Chromosome-level genome assembly of the humpback puffer, *Tetraodon palembangensis*. GigaByte (Hong Kong, China), 2021, gigabyte17.

Ding X, et al. (2020) Genome sequence of the agarwood tree *Aquilaria sinensis* (Lour.) Spreng: the first chromosome-level draft genome in the Thymelaeaceae family. GigaScience, 9(3).

Courtine D, et al. (2020) Long-read only assembly of *Drechmeria coniospora* genomes reveals widespread chromosome plasticity and illustrates the limitations of current nanopore methods. GigaScience, 9(9).

Safdar N, et al. (2020) Using Virus Sequencing to Determine Source of SARS-CoV-2 Transmission for Healthcare Worker. Emerging infectious diseases, 26(10), 2489.

Zeng X, et al. (2020) Genome sequencing of deep-sea hydrothermal vent snails reveals adaptations to extreme environments. GigaScience, 9(12).